

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	241	5 US-10-618-281-11	Sequence 11, App
2	1155.5	90.5	308	4 US-10-312-334-4	Sequence 4, Appli
3	1110.5	87.0	338	4 US-10-087-319-315	Sequence 315, App
4	1100.5	86.2	310	3 US-09-934-392-2	Sequence 2, Appli
5	1100.5	86.2	310	4 US-10-398-07-65	Sequence 65, Appli
6	1069.5	83.8	310	4 US-10-115-479-6	Sequence 6, Appli
7	1069.5	83.8	285	5 US-10-618-281-16	Sequence 16, Appli
8	1066.5	83.5	290	4 US-10-115-479-4	Sequence 4, Appli
9	1065	83.4	458	4 US-10-363-616-280	Sequence 280, App
10	1061	83.1	305	5 US-10-618-281-21	Sequence 21, Appli
11	1037.5	81.2	236	5 US-10-618-281-39	Sequence 39, Appli
12	1026.5	80.4	403	5 US-10-150-763-5838	Sequence 5833, A
13	954	74.7	286	6 US-11-097-143-24690	Sequence 24690, A
14	774	60.6	236	4 US-10-087-192-318	Sequence 318, App
15	665	52.1	244	6 US-11-197-143-32013	Sequence 32013, A
16	616.5	48.3	364	5 US-10-739-330-10670	Sequence 10670, A
17	607.5	47.6	367	4 US-10-425-115-345880	Sequence 345880,
18	603.5	47.3	305	4 US-10-125-115-296034	Sequence 296034,
19	597	46.8	389	4 US-10-437-363-111752	Sequence 111752,
20	594.5	46.6	383	4 US-10-4-115-201722	Sequence 201722,
21	594.5	46.6	452	4 US-10-425-114-60109	Sequence 60109, A
22	593.5	46.5	546	4 US-10-437-363-185558	Sequence 185558,
23	591.5	46.3	344	5 US-10-450-163-48788	Sequence 48788, A
24	581.5	45.5	395	4 US-10-437-363-180508	Sequence 180508,
25	578.5	45.3	415	4 US-10-425-114-67729	Sequence 67729, A
26	578.5	45.3	415	4 US-10-425-115-233872	Sequence 213872,
27	572.5	44.8	367	4 US-10-424-599-197073	Sequence 197073,

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1277	100.0	241	5 US-10-618-281-11	Sequence 11, App
2	1155.5	90.5	308	4 US-10-312-334-4	Sequence 4, Appli
3	1110.5	87.0	338	4 US-10-087-319-315	Sequence 315, App
4	1100.5	86.2	310	3 US-09-934-392-2	Sequence 2, Appli
5	1100.5	86.2	310	4 US-10-398-07-65	Sequence 65, Appli
6	1069.5	83.8	310	4 US-10-115-479-6	Sequence 6, Appli
7	1069.5	83.8	285	5 US-10-618-281-16	Sequence 16, Appli
8	1066.5	83.5	290	4 US-10-115-479-4	Sequence 4, Appli
9	1065	83.4	458	4 US-10-363-616-280	Sequence 280, App
10	1061	83.1	305	5 US-10-618-281-21	Sequence 21, Appli
11	1037.5	81.2	236	5 US-10-618-281-39	Sequence 39, Appli
12	1026.5	80.4	403	5 US-10-150-763-5838	Sequence 5833, A
13	954	74.7	286	6 US-11-097-143-24690	Sequence 24690, A
14	774	60.6	236	4 US-10-087-192-318	Sequence 318, App
15	665	52.1	244	6 US-11-197-143-32013	Sequence 32013, A
16	616.5	48.3	364	5 US-10-739-330-10670	Sequence 10670, A
17	607.5	47.6	367	4 US-10-425-115-345880	Sequence 345880,
18	603.5	47.3	305	4 US-10-125-115-296034	Sequence 296034,
19	597	46.8	389	4 US-10-437-363-111752	Sequence 111752,
20	594.5	46.6	383	4 US-10-4-115-201722	Sequence 201722,
21	594.5	46.6	452	4 US-10-425-114-60109	Sequence 60109, A
22	593.5	46.5	546	4 US-10-437-363-185558	Sequence 185558,
23	591.5	46.3	344	5 US-10-450-163-48788	Sequence 48788, A
24	581.5	45.5	395	4 US-10-437-363-180508	Sequence 180508,
25	578.5	45.3	415	4 US-10-425-114-67729	Sequence 67729, A
26	578.5	45.3	415	4 US-10-425-115-233872	Sequence 213872,
27	572.5	44.8	367	4 US-10-424-599-197073	Sequence 197073,

RESULT 2

ALIGNMENTS

RESULT 1

US-10-618-281-11

; Sequence 11, Application US-10618281

; Publication No. US2004021969A1

; GENERAL INFORMATION:

; APPLICANT: Day, Anthony G.

; APPLICANT: Estell, David A.

; APPLICANT: Lyons, Eric H.

; APPLICANT: Yao, Jian

; TITLE OF INVENTION: Previously Known as Proteases Not Modulating Proteins

; CURRENT FILING DATE: 2003-07-11

; CURRENT APPLICATION NUMBER: US-10/618,281

; PRIOR APPLICATION NUMBER: US 60/395,325

; SEQ ID NO: 92

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 11

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-618-281-11

Query Match 100.0%; Score 1277; DB 5;

Best Local Similarity 100.0%; Pred. No. 1.2e-128;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Caps 0;

1 SLHLISERADQYSQFELDAVEFFRTARDNRLGMFVRCPASSRTLLFSGHNAVDLGQ 60

1 SLHLISERADQYSQFELDAVEFFRTARDNRLGMFVRCPASSRTLLFSGHNAVDLGQ 60

1 SLHLISERADQYSQFELDAVEFFRTARDNRLGMFVRCPASSRTLLFSGHNAVDLGQ 60

61 MCSFYIGLGSRINCNTFSYDGSYGSCKPSEKQNLYADDAWQNLRTYGVSPNII 120

61 MCSFYIGLGSRINCNTFSYDGSYGSCKPSEKQNLYADDAWQNLRTYGVSPNII 120

121 YQSIGTGTVPITDLSRYECAVILHSPLMGSLRVAFPDTRXTCFDAFPSPIDKISVTPSP 180

121 YQSIGTGTVPITDLSRYECAVILHSPLMGSLRVAFPDTRXTCFDAFPSPIDKISVTPSP 180

181 VLVHGTEDEVDFSHGLMYERCRAVEPLWEGAHNDIELYACYLERLKQFHLPN 240

181 VLVHGTEDEVDFSHGLMYERCRAVEPLWEGAHNDIELYACYLERLKQFHLPN 240

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GenCore version 5.1.6

OM protein - protein search, using bw model

Run on: November 21, 2005, 12:07:52 ; Search time 188 Seconds (without alignments)

563-246 Million cell updates/sec

Title: US-10-618-281-11

Perfect score: 1277

Sequence: 1 SLHLSERADWQYSQRELDAY.....ELYAQYLERLKQFIHELPNS 241

Scoring table: BLOSUM62

Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqP19800:*

2: geneseqP19900:*

3: geneseqP20000:*

4: geneseqP20018:*

5: geneseqP20021:*

6: geneseqP2003aB:*

7: geneseqP2003bB:*

8: geneseqP2004a:*

9: geneseqP2005a:*

RESULT 1

ADU24063 ID ADU24063 standard; protein; 241 AA.

XX AC

XX DT 27-JAN-2005 (first entry)

XX DE Human serine peptidase enzyme #3.

XX DS Human

XX KW protease; cancer; immune-related disorder; cardiovascular disease; brain-associated disease; neuronal-associated disease; metabolic disorder; haematopoietic; cytostatic; immunosuppressive; cardiovascular; cerebroprotective; neuroprotective; human; serine peptidase; enzyme; peripheral nervous system; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypertension; hypertension; psychotic disorder; neurological disorder; dyskinesia; organ transplant rejection.

XX OS Homo sapiens.

XX PH Key

XX FT Domain

36 . 240 /note = Protease active domain

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	1277	100.0	241	8	ADU24063	Adu24063 Human ser
2	1266.5	99.2	242	8	ADN05213	Adn05213 Antipsoni
3	1266.5	99.2	329	8	ADK71002	Adk71002 Human est
4	1259.5	98.6	322	8	ADS10621	AdS10621 Human est
5	1259.5	98.6	329	8	ADS10620	AdS10620 Human the
6	1252.5	98.1	247	7	ADF60194	Adf60194 Human con
7	1252.5	98.1	247	8	ADS11892	AdS11892 Human the
8	1252.5	98.1	247	8	ADS11891	AdS11891 Human the
9	1155.5	90.5	308	5	AAU81978	Aau81978 Human sec
10	1110.5	87.0	338	7	ABM85300	Abm85300 Mouse pro
11	1100.5	86.2	310	4	AAM93226	Aam93226 Human pol
12	1100.5	86.2	310	5	AAU77137	Aau77137 Human alp
13	1100.5	86.2	310	5	ABP43541	Abp43541 Human sec
14	1100.5	86.2	310	8	ADL30608	Adl30608 Human pro
15	1095.5	85.8	310	7	ADE15976	Ade15976 G-coupled
16	1095.5	85.8	310	8	ADL39195	Adl39195 Human G-c
17	1066.5	85.0	293	8	ADL21199	Adl21199 Amn/ac
18	1069.5	83.8	285	8	ADU24068	Adu24068 Human ser
19	1066.5	83.5	290	7	ADE15974	Ade15974 G-coupled
20	1066.5	83.5	290	8	ADL93913	Adl93913 Human G-c
21	1066.5	83.5	361	8	ABM80127	Abm80127 Tumour-as
22	1065	83.4	361	8	ADG20182	Adg20182 Human PRO
23	1065	83.4	361	8	ABM81992	Abm81992 Tumour-as
24	1065	83.4	458	5	ABP62843	Abp62843 Human pol

Identifying compound that modulates activity of protease, by contacting protease with test compound, measuring activity of protease before and after contacting step, and determining whether test compound modulates

ALIGNMENTS

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:20:17 ; Search time 16 Seconds
 Sequence: 1 SLHLSERADWQYSQRELDAY.....ELYAQYLERLKOFIHELPNS 241
 Scoring table: BLOSUM62
 Gapext 0.5
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 80:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	825.5	64.6	405	T23321	hypothetical prote
2	586.5	45.9	365	T05558	hypothetical prote
3	571.5	44.8	369	T48612	hypothetical prote
4	545.5	42.7	341	B86269	F2123.4 protein -
5	534.5	41.9	422	D86446	hypothetical prote
6	525.5	41.2	316	C84635	hypothetical prote
7	481.5	37.9	256	G96692	hypothetical prote
8	462	36.2	307	C85363	hypothetical prote
9	399	31.2	245	AD2564	hypothetical prote
10	363.5	28.5	305	T20470	hypothetical prote
11	323.5	25.3	335	T20465	hypothetical prote
12	239.5	18.8	281	G70734	hypothetical prote
13	213.5	16.7	293	E65030	hypothetical prote
14	207.5	16.2	293	C85898	probable proteinas
15	207.5	16.2	293	H91053	probable enzyme [i
16	202	15.8	284	S51294	probable membrane
17	189.5	14.8	292	AB08225	RTX toxin RTxA VC1
18	159.5	12.5	247	T17237	hydrolase - Strept
19	150	11.7	301	G83192	2-hydroxy-6-oxohep
20	138	10.8	254	C95273	arylester hydrolas
21	134.5	10.5	482	S44638	dipeptidyl peptida
22	131.5	10.3	251	AD3177	probable lipase
23	131.5	10.3	251	AP2674	lysophospholipase
24	122.5	9.6	4558	C82199	lysophospholipase
25	122	9.6	261	T26708	lysophospholipase
26	120.5	9.4	239	C69334	lysophospholipase
27	118.5	9.3	302	AB3196	lysophospholipase
28	116	9.1	282	G75384	lysophospholipase
29	116	9.1	318	T00552	lysophospholipase

30	114	8.9	330	2	D97235
	112.5	8.8	340	2	TS1482
	111.5	8.7	283	2	B87546
	111.5	8.7	378	2	T41456
	111.5	8.6	305	2	F69965
	110	8.5	305	2	F86821
	108.5	8.5	289	2	S73722
	107.5	8.4	264	2	H75406
	107.5	8.4	319	2	T47658
	106.5	8.3	319	2	A11704
	106.5	8.3	321	2	D83813
	106.5	8.2	339	2	C83606
	106.5	8.2	339	2	AB6640
	105.5	8.3	311	2	T60717
	104.5	8.1	459	2	TS1482
	103.5	8.1	459	2	T04911
	102.5	8.0	471	2	TS1482
	102	8.0	304	2	T02661

ALIGNMENTS

Accession: 123321
R;Gardner, A.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19727
A;Accession: T23321
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-105 <WIL>
A;Cross-references: UNIPROT:Q21221; UNIPARC:UPI000007E914;
A;Experimental source: clone K04622
PIDN:C

Result No.	Score	Query Match	Length	DB ID	Description
1	825.5	64.6	405	2	hypothetical prote
2	586.5	45.9	365	2	hypothetical prote
3	571.5	44.8	369	2	hypothetical prote
4	545.5	42.7	341	2	F21P23.4 protein -
5	534.5	41.9	422	2	hypothetical prote
6	525.5	41.2	316	2	hypothetical prote
7	481.5	37.7	256	2	hypothetical prote
8	462	36.2	307	2	hypothetical prote
9	399	31.2	245	2	hypothetical prote
10	363.5	28.5	305	2	hypothetical prote
11	323.5	25.3	335	2	hypothetical prote
12	239.5	18.8	281	2	hypothetical prote
13	213.5	16.7	293	2	hypothetical prote
14	207.5	16.2	293	2	probable proteinas
15	207.5	16.2	293	2	probable enzyme
16	202	15.8	284	2	probable membrane
17	189.5	14.8	292	2	probable membrane
18	159.5	12.5	247	2	hypothetical prote
19	150	11.7	301	2	hypothetical prote
20	138	10.8	254	2	hypothetical prote
21	134.5	10.5	482	2	hypothetical prote
22	131.5	10.3	251	2	ATTS protein (imp)
23	131.5	10.3	4558	2	RTX toxin RTxA VC1
24	122.5	9.6	261	2	hydrolase - Strept
25	122	9.6	238	2	2-hydroxy-6-oxohep
26	120.5	9.4	302	2	ary ester hydrolas
27	118.5	9.3	251	2	dipeptidyl peptida
28	116	9.1	282	2	probable lipase
29	116	9.1	318	2	lysophospholipase

Query	Match	64.6%	Score	825.5	DB	2	Length	405	
Best Local	Similarity	66.1%	Pred. No.	5.4e-06					
Matches	152;	Conservative	36;	Mismatches	41;	Indels	1;	Gaps	1
YY	7	RADWQYSQREL-DAVEFFESRTARDNRLGCMFVRCAPSSRYTLLFSGHNAVDLGQMSCSFY	65						
Db	146	RAAWPHOEVDMANCVENRIRTRRARRVACTMIRPENSHTELLFSGHNAVDLGQMTSFL	205						
YY	66	IGLGSRINCNIFPSYDGSYGYSSGKSEKNUYADIAAWQQLRTRKGVSPENILLYGQSI	125						
Db	206	YLGFGHINCNVFSYDGSYGYCSTGKSEKNUYADTTAAPELJKSEFGVPEKEKILLYGQSI	265						
YY	126	GTVPTYDLASRYECAAVLHSPMSGLRVAFDTRKTYCFDADPSIDKISKWTSPVLYIIVH	185						
Db	266	GTVPSYDLASREBLLAULVHSPMSGMRAVPGTTIWCCDADPSIBKVRVCKPTLVIIH	325						
YY	186	GTEDEVIDFSGHGLMYERCRAPEP1WVEGFGHND1ELYAOYLERLKQF1	235						
Db	326	GTDDEVIDFSGHSGVSYBRCPTSPVRYWPGFGHGNVDRUHAYFRBPSF1	375						

RESULT 2
T05558 hypothetical protein F22K18.40 - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 2-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05558
C;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Newes, H.W.; M
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15419
A;Accession: T05558
A;Molecule type: DNA

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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:33:53 ; Search time 46 Seconds (without alignments)

433.149 Million cell updates/sec

Title: US-10-618-281-11

Prefect score: 1277

Sequence: 1 STHLSERADWQYSQRELDAY.....ELYAQYLERLKQFIHELPNS 241

Scoring table: BL03062 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 8265679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing First 45 summaries

Database : Issued Patents AA:^{*}

1: /cgn2_6/_ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/_ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/_ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/_ptodata/1/iaa/PCUTS_COMB.pep:*

5: /cgn2_6/_ptodata/1/iaa/RB_COMB.pep:*

6: /cgn2_6/_ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	943.5	73.9	374	2 US-09-270-767-45545	Sequence 45545, A
2	286	22.4	152	2 US-09-270-767-61054	Sequence 61054, A
3	227	17.8	263	2 US-09-248-798A-12703	Sequence 12703, A
4	184.5	14.4	275	2 US-09-248-798A-15244	Sequence 15244, A
5	150	11.7	661	2 US-09-252-991A-18225	Sequence 18225, A
6	149.5	11.7	312	2 US-09-107-532A-5684	Sequence 5684, AP
7	126.5	9.9	2807	2 US-09-543-680A-4980	Sequence 4980, AP
8	118.5	9.3	339	2 US-19-489-847-7350	Sequence 350, APP
9	118.5	9.3	554	2 US-09-489-847-7352	Sequence 352, APP
10	117.5	9.2	398	2 US-09-107-532A-6418	Sequence 6418, AP
11	110	8.6	305	2 US-09-162-845-9	Sequence 9, Appli
12	110	8.6	305	2 US-10-402-312-9	Sequence 9, Appli
13	110	8.6	305	2 US-10-401-437-9	Sequence 9, Appli
14	110	8.6	305	2 US-10-402-067-9	Sequence 9, Appli
15	110	8.6	305	2 US-10-401-436-9	Sequence 9, Appli
16	109.5	8.6	271	2 US-09-710-279-2822	Sequence 2822, AP
17	109.5	8.6	271	2 US-09-710-279-3308	Sequence 3308, AP
18	107	8.4	284	2 US-09-134-001C-2927	Sequence 2927, AP
19	106.5	8.3	300	2 US-09-555-166-4	Sequence 4, Appli
20	106.5	8.3	374	2 US-09-552-991A-27773	Sequence 27773, A
21	106	8.3	296	2 US-09-902-540-6002	Sequence 10861, A
22	100	7.8	346	1 US-08-002-359A-34	Sequence 34, Appli
23	99.5	7.8	255	2 US-09-489-039A-9075	Sequence 9075, AP
24	98.5	7.7	297	1 US-08-502-550-10571	Sequence 37, Appli
25	95	7.4	298	1 US-09-328-350-7313	Sequence 7313, AP
26	93.5	7.3	310	2 US-09-228-350-7313	Sequence 31105, A
27	93.5	7.3	589	2 US-09-252-991A-31105	Sequence 31105, A

ALIGNMENTS

RESULT 1
US-09-270-767-45545
; Sequence 45545, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 45545
; LENGTH: 374

; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-45545

Query Match 73.9%; Score 943.5; DB 2; Length 374;
Best Local Similarity 72.0%; Mismatches 37; Indels 1; Gaps 1;
Matches 170; Conservative

Qy 1 SLHLSPRADWQYSORELDAVEFFSRTARDNRLGCMFVRCPASSRYTLLFSGHGNAYDLGQ 60
Db 54 NLQLPDRAEWQSYERKSKVEAFFTRTSRGNLITCIVYRCSKNAKYTLFSGHGNAYDLGQ 113

Qy 61 MCSPIYGLSRSPINCNFSYDPSYGSYGSKSEKVNAYDIDAWQQL-RTRYGVSPPNII 119
Db 114 MSSFYLTLGSQLINCNFPGYDPSYGSYGSKSEKVNAYDIDAAWQXMRTRFNISPETII 173

Qy 120 LYQSQSITGVPTVLDLARYECAVILSPLMSLGLRVAFLPDTTRKTCFADPSIDKISKVTS 179
Db 174 LYQSQSITGVPTVLDLARYECAVILSPLMSLGLRVAFLPDTTRKTCFADPSIDKISKVTS 233

Qy 180 PVLVIGTGEDEVIDFSGHGLAMYCRPRAVEPLWVEAGHNDIELYAOYLERLKOFI 235
Db 234 PVLVIGTGEDEVIDFSGHGLAMYCRPRAVEPLWVEAGHNDVELHPHYERLRLKFL 289

RESULT 2
US-09-270-767-61054
; Sequence 61054, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

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OM protein - protein search, using SW model

Run on: November 21, 2005, 12:37:13 ; Search time 6 Seconds (without alignments)

45.380 Million cell updates/sec

Title: US-10-618-281-11

Perfect score: 1277

Sequence: 1 SLHLSBRADWQYSQRELDAY.....ELYAQYLERLQKQFTHLPNS 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing first 45 summaries

Database : Published Applications AA_New:*

1: /cgn2_6/ptodata/2/pubpaa/us10_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/us06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/us07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/us08_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/us09_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/us11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/us60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1

US-11-179-977-4

; Sequence 4, Application US/11179977

; Publication No. US2005024978A1

; APPLICANT: Genencor International, Inc.

; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes

; FILE REFERENCE: GCS11_PCT

; CURRENT APPLICATION NUMBER: US/11/179, 977

; CURRENT FILING DATE: 2005-07-12

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 4

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Bacillus

; US-11-179-977-4

ALIGNMENTS

Query Match 8.4% ; Score 107; DB 7; Length 300;

Best Local Similarity 21.7% ; Pred. No. 2 9e-05; Mismatches 94; Indels 42; Gaps 11;

Matches 49; Conservative 41; Gaps 11;

Qy 47 TLLFSGG--NAVDLGCMCSFYIGLGSRINCNIFSYDGSYGVSSCKPSEKKNLYA--DID 101

Db 83 TIIICHGTVNVLNSLKYMHFLDLG---WNVLITYDHRIGQSGGRTTISGFYEBKDLN 138

Qy 102 AAWQALRTRYGVSPENI-LXGQSIGTVPV---DLSRYY-EECAAVLHSLLMS 150

Db 139 KVVSUJNK--TNHRCUIGIHGEMSMAVTALLYAGAHCSGDAFYIADCPCFACFDQLAY 196

Qy 151 GLRVA--FPDTRKTYCFDAPSPIDKISKVTPVWHTGTEDEVDFSH 196

Db 197 RRAEAYLPSNPLPAPAFFKLKGYYTAREVSPLAVTDIEKPVLTISKDDYIPVSS 256

RESULT 2

US-11-179-977-2

; Sequence 2, Application US/11179977

; Publication No. US2005024978A1

; APPLICANT: Genencor International, Inc.

; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes

; FILE REFERENCE: GCS11_PCT

; CURRENT APPLICATION NUMBER: US/11/179, 977

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	107	8.4	300	7	US-11-179-977-4	Sequence 4, Appli
2	78	6.1	256	7	US-11-179-977-2	Sequence 2, Appli
3	74	5.8	872	7	US-11-077-550-145	Sequence 145, Appli
4	69.5	5.4	319	7	US-11-109-156-38	Sequence 38, Appli
5	69.5	5.4	323	7	US-11-103-156-37	Sequence 37, Appli
6	68.5	5.4	242	7	US-11-179-977-14	Sequence 14, Appli
7	65.5	5.1	330	1	US-10-689-742-82	Sequence 82, Appli
8	65.5	5.1	657	7	US-11-179-977-1	Sequence 1, Appli
9	64	5.0	269	7	US-11-179-977-11	Sequence 11, Appli
10	63.5	5.0	325	7	US-11-074-176-370	Sequence 370, Appli
11	63	5.0	429	7	US-11-076-248	Sequence 248, Appli
12	63	4.9	298	7	US-11-109-156-34	Sequence 34, Appli
13	60	4.7	211	7	US-11-179-977-6	Sequence 6, Appli
14	59.5	4.7	520	7	US-11-098-662-12	Sequence 12, Appli
15	59.5	4.7	799	7	US-11-098-662-16	Sequence 38, Appli
16	59.5	4.7	805	7	US-11-074-176-172	Sequence 172, Appli
17	59	4.6	119	1	US-10-145-25	Sequence 25, Appli
18	59	4.6	256	7	US-11-179-977-15	Sequence 15, Appli
19	59	4.6	318	7	US-11-179-977-16	Sequence 16, Appli
20	58.5	4.6	211	7	US-11-098-662-16	Sequence 4, Appli
21	58.5	4.6	2376	7	US-11-098-662-16	Sequence 2, Appli
22	58.5	4.6	2715	7	US-11-098-651-4	Sequence 21, Appli
23	58	4.5	2280	7	US-11-077-562-11	Sequence 82, Appli
24	57.5	4.5	876	7	US-11-077-550-82	Sequence 18, Appli
25	57.5	4.5	1332	7	US-11-091-643-18	